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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658C

DATE: 08/06/2002

TIME: 17:02:16

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Output Set: N:\CRF3\08062002\I729658C.raw

P.6

3 <110> APPLICANT: Zonana et al.  
 5 <120> TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins  
 7 <130> FILE REFERENCE: 55924  
 9 <140> CURRENT APPLICATION NUMBER: 09/729,658C  
 10 <141> CURRENT FILING DATE: 2000-12-04  
 12 <150> PRIOR APPLICATION NUMBER: 09/342,681  
 13 <151> PRIOR FILING DATE: 1999-06-29  
 15 <150> PRIOR APPLICATION NUMBER: 60/092,279  
 16 <151> PRIOR FILING DATE: 1998-07-09  
 18 <150> PRIOR APPLICATION NUMBER: 60/112,366  
 19 <151> PRIOR FILING DATE: 1998-12-15  
 21 <160> NUMBER OF SEQ ID NOS: 127  
 23 <170> SOFTWARE: PatentIn Ver. 2.1  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 1574  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Homo sapiens  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (242)..(1417)  
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 37 cggagtagaa ctgcacatgc ggctgtccccc tgctccgtcc cggccagcca ctgtcgcgca 120  
 39 ggaacgggtc cctgcagccc ccagccgatg gcaggacagt agccgcctgt cagaggctgt 180  
 41 gaacggctga ggcagacgcga ggggtctcccg ggcctcaaga gagtgggtgt ctccggaggc 240  
 43 c atg ggc tac ccg gag gtg gag cgc agg gaa ctc ctg cct gca gca gcg 289  
 44 Met Gly Tyr Pro Glu Val Glu Arg Arg Glu Leu Leu Pro Ala Ala Ala  
 45 1 5 10 15  
 47 ccg cgg gag cga ggg agc cag ggc tgc ggg tgt ggc ggg gcc cct gcc 337  
 48 Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Gly Gly Ala Pro Ala  
 49 20 25 30  
 51 cgg gcg ggc gaa ggg aac agc tgc ctg ctc ttc ctg ggt ttc ttt ggc 385  
 52 Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly  
 53 35 40 45  
 55 ctc tcg ctg gcc ctc cac ctg ctg acg ttg tgc tgc tac cta gag ttg 433  
 56 Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu  
 57 50 55 60  
 59 cgc tcg gag ttg cgg cgg gaa cgt gga gcc gag tcc cgc ctt ggc ggc 481  
 60 Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly  
 61 65 70 75 80  
 63 tcg ggc acc cct ggc acc tct ggc acc cta agc agc ctc ggt ggc ctc 529  
 64 Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu  
 65 85 90 95

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67 gac cct gac agc ccc atc acc agt cac ctt ggg cag ccg tca cct aag	577
68 Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys	
69 100 105 110	
71 cag cag cca ttg gaa ccg gga gaa gcc gca ctc cac tct gac tcc cag	625
72 Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln	
73 115 120 125	
75 gac ggg cac cag atg gcc cta ttg aat ttc ttc ctc gat gaa aag	673
76 Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys	
77 130 135 140	
79 cca tac tct gaa gaa gaa agt agg cgt gtt cgc cgc aat aaa aga agc	721
80 Pro Tyr Ser Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser	
81 145 150 155 160	
83 aaa agc aat gaa gga gca gat ggc cca gtt aaa aac aag aaa aag gga	769
84 Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly	
85 165 170 175	
87 aag aaa gca gga cct cct gga ccc aat ggc cct cca gga ccc cca gga	817
88 Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly	
89 180 185 190	
91 cct cca gga ccc cag gga ccc cca gga att cca ggg att cct gga att	865
92 Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile	
93 195 200 205	
95 cca gga aca act gtt atg gga cca cct ggt cct cca ggt cct cct ggt	913
96 Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly	
97 210 215 220	
99 cct caa gga ccc cct ggc ctc cag gga cct tct gtt gct gct gat aaa	961
100 Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys	
101 225 230 235 240	
103 gct gga act cga gaa aac cag cca gct gtg gtg cat cta cag ggc caa	1009
104 Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln	
105 245 250 255	
107 ggg tca gca att caa gtc aag aat gat ctt tca ggt gga gtg ctc aat	1057
108 Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn	
109 260 265 270	
111 gac tgg tct cgc atc act atg aac ccc aag gtg ttt aag cta cat ccc	1105
112 Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro	
113 275 280 285	
115 cgc agc ggg gag ctg gag gta ctg gtg gac ggc acc tac ttc atc tat	1153
116 Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr	
117 290 295 300	
119 agt cag gta gaa gta tac tac atc aac ttc act gac ttt gcc agc tat	1201
120 Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr	
121 305 310 315 320	
123 gag gtg gtg gtg gat gag aag ccc ttc ctg cag tgc aca cgc agc atc	1249
124 Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile	
125 325 330 335	
127 gag acg ggc aag acc aac tac aac act tgc tat acc gca ggc gtc tgc	1297
128 Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys	
129 340 345 350	
131 ctc ctc aag gcc cgg cag aag atc gcc gtc aag atg gtg cac gct gac	1345

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132 Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp  
 133 355 360 365  
 135 atc tcc atc aac atg agc aag cac acc acg ttc ttt ggg gcc atc agg 1393  
 136 Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg  
 137 370 375 380  
 139 ctg ggt gaa gcc cct gca tcc tag attccccat tttgcctctg tccgtgcccc 1447  
 140 Leu Gly Glu Ala Pro Ala Ser 1447  
 141 385 390  
 143 ttccctgggt ttgggagcca ggactccaa aacctctaag tgctgctgtg gagtgaggtg 1507  
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 152 <212> TYPE: PRT  
 153 <213> ORGANISM: Homo sapiens  
 155 <400> SEQUENCE: 2  
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 158 Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Gly Ala Pro Ala  
 159 20 25 30  
 160 Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly  
 161 35 40 45  
 162 Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu  
 163 50 55 60  
 164 Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly  
 165 65 70 75 80  
 166 Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu  
 167 85 90 95  
 168 Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys  
 169 100 105 110  
 170 Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln  
 171 115 120 125  
 172 Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys  
 173 130 135 140  
 174 Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser  
 175 145 150 155 160  
 176 Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly  
 177 165 170 175  
 178 Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly  
 179 180 185 190  
 180 Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile  
 181 195 200 205  
 182 Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly  
 183 210 215 220  
 184 Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys  
 185 225 230 235 240  
 186 Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln  
 187 245 250 255  
 188 Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn

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Input Set : A:\55924.app

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190 Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro			
191 275	280	285	
192 Arg Ser Gly Glu Leu Glu Val Val Asp Gly Thr Tyr Phe Ile Tyr			
193 290	295	300	
194 Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr			
195 305	310	315	320
196 Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile			
197 325	330	335	
198 Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys			
199 340	345	350	
200 Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp			
201 355	360	365	
202 Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg			
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212 <213> ORGANISM: Mus musculus			
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215 <221> NAME/KEY: CDS			
216 <222> LOCATION: (142)..(1275)			
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223 tagtggttgt ctctggaggc c atg ggc tac cca gag gta gag cgc agg gaa 171			
224 Met Gly Tyr Pro Glu Val Glu Arg Arg Glu			
225 1 5 10			
227 ccc ctg cct gcg gca gcg cca agg gag cgg ggc agc cag ggc tgc ggc 219			
228 Pro Leu Pro Ala Ala Ala Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly			
229 15 20 25			
231 tgt cgc ggg gcc cct gct cgg gcg ggc gaa ggg aac aac tgc cgg ctc 267			
232 Cys Arg Gly Ala Pro Ala Arg Ala Gly Glu Gly Asn Ser Cys Arg Leu			
233 30 35 40			
235 ttc ctg ggt ttc ttt ggc ctc tcg ctg gcc ctc cac ctg ctg acg ctg 315			
236 Phe Leu Gly Phe Gly Leu Ser Leu Ala Leu His Leu Leu Thr Leu			
237 45 50 55			
239 tgc tgc tac cta gag ttg cgg tcc gaa ttg cgg cgg gaa cgg gga acc 363			
240 Cys Cys Tyr Leu Glu Leu Arg Ser Glu Leu Arg Arg Glu Arg Gly Thr			
241 60 65 70			
243 gag tcc cgc ctc ggt ggc ccc ggt gct cct ggc acc tct ggc acc cta 411			
244 Glu Ser Arg Leu Gly Gly Pro Gly Ala Pro Gly Thr Ser Gly Thr Leu			
245 75 80 85 90			
247 agc agc cct ggg agc ctc gac ccc ggt gct ccc atc acc cgc cac ctg 459			
248 Ser Ser Pro Gly Ser Leu Asp Pro Val Gly Pro Ile Thr Arg His Leu			
249 95 100 105			
251 ggg cag ccg tcc ttt caa cag cag cct ttg gaa ccg gga gaa gat cca 507			

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253					110				115							120	
255	ctc	ccc	cct	gag	tcc	cag	gac	cg	ca	cag	atg	gcc	ctc	ctg	aat	tcc	
256	Leu	Pro	Pro	Glu	Ser	Gln	Asp	Arg	His	Gln	Met	Ala	Leu	Leu	Asn	Phe	
257					125				130							135	
259	tcc	ttt	cct	gat	gaa	aag	gca	tat	tct	gaa	gag	gaa	agt	agg	cgt	gtt	
260	Phe	Phe	Pro	Asp	Glu	Lys	Ala	Tyr	Ser	Glu	Glu	Glu	Ser	Arg	Arg	Val	
261					140				145							150	
263	cgc	cgc	aat	aag	aga	aga	agc	aaa	agt	ggt	gaa	gga	gca	gat	ggt	cct	gtt
264	Arg	Arg	Asn	Lys	Arg	Ser	Lys	Ser	Gly	Glu	Gly	Ala	Asp	Gly	Pro	Val	
265	155								160							165	
267	aaa	aaa	aac	aag	aaa	aag	gga	aag	gca	ggg	cca	cct	ggg	ccc	aat	ggc	
268	Lys	Asn	Lys	Lys	Lys	Gly	Lys	Lys	Ala	Gly	Pro	Pro	Gly	Pro	Asn	Gly	
269									175							180	
271	ccc	cca	gga	cct	cca	gga	cct	ccg	gga	ccc	cag	gga	cct	cca	ggg	att	
272	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Gln	Gly	Pro	Pro	Gly	Ile	
273					190				195							200	
275	cca	gga	att	cct	ggg	att	cca	gga	aca	act	gtt	atg	gga	cca	cct	ggc	
276	Pro	Gly	Ile	Pro	Gly	Ile	Pro	Gly	Thr	Thr	Val	Met	Gly	Pro	Pro	Gly	
277					205				210							215	
279	cca	cct	ggc	cct	cct	ggt	cct	caa	gga	ccc	cct	ggc	ctc	caa	gga	cct	
280	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Gln	Gly	Pro	Pro	Gly	Leu	Gln	Gly	Pro	
281					220				225							230	
283	tct	gg	gt	gt	gt	gt	aaa	act	gga	act	cg	gaa	aat	cag	cca	gct	gt
284	Ser	Gly	Ala	Ala	Asp	Lys	Thr	Gly	Thr	Arg	Glu	Asn	Gln	Pro	Ala	Val	
285	235					240				245						250	
287	gt	gt	cat	ctg	cag	ggc	caa	ggg	tca	gca	att	caa	gtc	aaa	aat	gat	ctt
288	Val	His	Leu	Gln	Gly	Gln	Gly	Ser	Ala	Ile	Gln	Val	Lys	Asn	Asp	Leu	
289						255				260						265	
291	tca	gg	gt	gt	gt	ctc	aat	gac	tgg	tct	cg	atc	act	atg	aa	cct	aa
292	Ser	Gly	Gly	Val	Leu	Asn	Asp	Trp	Ser	Arg	Ile	Thr	Met	Asn	Pro	Lys	
293					270				275							280	
295	gt	ttt	aaa	cta	cat	ccc	cgc	agc	ggg	gag	ctg	gag	gtc	tac	tac	atc	
296	Val	Phe	Lys	Leu	His	Pro	Arg	Ser	Gly	Glu	Leu	Glu	Val	Tyr	Tyr	Ile	
297					285				290							295	
299	aac	tcc	act	gac	ttt	gcc	agc	tac	gag	gt	gt	gt	gt	gat	gag	aag	ccc
300	Asn	Phe	Thr	Asp	Phe	Ala	Ser	Tyr	Glu	Val	Val	Val	Asp	Glu	Lys	Pro	
301					300				305							310	
303	tcc	ctg	cag	tgc	acc	cgc	agc	att	gag	aca	ggg	aag	acc	aa	cc	ttc	
304	Phe	Leu	Gln	Cys	Thr	Arg	Ser	Ile	Glu	Thr	Gly	Lys	Thr	Asn	Tyr	Asn	
305	315					320				325						330	
307	act	tgc	tat	act	gca	ggc	gt	tgc	ctc	ctc	aag	gcc	agg	cag	aaa	atc	
308	Thr	Cys	Tyr	Thr	Ala	Gly	Val	Cys	Leu	Leu	Lys	Ala	Arg	Gln	Lys	Ile	
309						335				340						345	
311	gcc	gt	aag	atg	gt	cac	gt	gac	atc	tct	atc	aat	atg	agc	aag	cac	
312	Ala	Val	Lys	Met	Val	His	Ala	Asp	Ile	Ser	Ile	Asn	Met	Ser	Lys	His	
313						350				355						360	
315	acc	acc	tcc	tcc	ggg	gcc	atc	agg	ctg	ggc	gaa	gcc	cct	gca	tcc	tag	
316	Thr	Thr	Phe	Phe	Gly	Ala	Ile	Arg	Leu	Gly	Glu	Ala	Pro	Ala	Ser		

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 65  
Seq#:9; N Pos. 754  
Seq#:11; N Pos. 302  
Seq#:12; N Pos. 2961,3423,3673  
Seq#:43; N Pos. 39  
Seq#:95; N Pos. 133,168,212,239,280,427,428,429  
Seq#:97; N Pos. 453,533,579  
Seq#:101; N Pos. 330,331,337,357,368,379,380,383,394,395,398,401,417,419  
Seq#:101; N Pos. 423,434,435,436,442,443,447,448,450,452,454,457,460,462  
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Seq#:113; N Pos. 210,213,219,222,225  
Seq#:115; N Pos. 8,9,16,26,37,41,54,60,61,62,83,88,92,95,98,100,102,105,109  
Seq#:115; N Pos. 114,117,123,131,139,141,144,148,154,155,157,165,171,177  
Seq#:115; N Pos. 185,187,188,189,193,202,204  
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